RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _09/845,157A_

Source: _1Fw16_

Date Processed by STIC: _10/18/04_

ENTERED

RAW SEQUENCE LISTING   DATE: 10/18/2004
PATENT APPLICATION: US/09/845,157A   TIME: 10:38:02

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\10182004\I845157A.raw

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 5 <110> APPLICANT: Smith, Michael D.
 6         Potter, Robert J.
 7         Dhariwal, Gulshan
 8         Gerard, Gary F.
 9         Rosenthal, Kim
12 <120> TITLE OF INVENTION: Thermostable Reverse Transcriptases and Uses Thereof
16 <130> FILE REFERENCE: 0942.5040001/RWE/MTT
20 <140> CURRENT APPLICATION NUMBER: US 09/845,157A
22 <141> CURRENT FILING DATE: 2001-05-01
26 <150> PRIOR APPLICATION NUMBER: US 60/207,196
28 <151> PRIOR FILING DATE: 2000-05-26
32 <160> NUMBER OF SEQ ID NOS: 8
36 <170> SOFTWARE: PatentIn version 3.0
40 <210> SEQ ID NO: 1
42 <211> LENGTH: 2151
44 <212> TYPE: DNA
46 <213> ORGANISM: Moloney-Murine Leukemia Virus
49 <220> FEATURE:
51 <221> NAME/KEY: CDS
53 <222> LOCATION: (1)..(2151)
56 <400> SEQUENCE: 1
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58 Met Gly Gly Ser His His His His His His Gly Met Ala Ser Met Thr
59 1               5                   10                  15
61 ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag cat       96
62 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys His
63             20                  25                  30
65 atg acc cta aat ata gaa gat gag tat cgg cta cat gag acc tca aaa      144
66 Met Thr Leu Asn Ile Glu Asp Glu Tyr Arg Leu His Glu Thr Ser Lys
67         35                  40                  45
69 gag cca gat gtt tct cta ggg tcc aca tgg ctg tct gat ttt cct cag      192
70 Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
71     50                  55                  60
73 gcc tgg gcg gaa acc ggg ggc atg gga ctg gca gtt cgc caa gct cct      240
74 Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro
75 65                  70                  75                  80
77 ctg atc ata ctt ctg aaa gca acc tct acc ccc gtg tcc ata aaa caa      288
78 Leu Ile Ile Leu Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
79                 85                  90                  95
81 tac ccc atg tca caa gaa gcc aga ctg ggg atc aag ccc cac ata cag      336
82 Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
83             100                 105                 110
85 aga ctg ttg gac cag gga ata ctg gta ccc tgc cag tcc ccc tgg aac      384
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86 Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn
87         115             120             125
89 acg ccc ctg cta ccc gtc aag aaa ccc ggg act aat gat tac agg cct      432
90 Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro
91      130             135             140
93 gtc caa gat ctg aga gag gtc aac aaa cgc gta gaa gac atc cac ccc      480
94 Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro
95 145             150             155                 160
97 acc gta ccc aac ccc tac aac ctc ttg agt ggg ctc cca ccg tcc cac      528
98 Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His
99             165             170             175
101 cag tgg tac act gtt cta gac tta aaa gat gcc ttt ttc tgc ctg aga      576
102 Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg
103            180             185             190
105 ctc cac ccg acg tct cag cct ctc ttc gcc ttt gaa tgg aga gac cca      624
106 Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro
107            195             200             205
109 gag atg gga atc tct ggc caa cta acc tgg acc aga ctc cca cag gga      672
110 Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly
111      210             215             220
113 ttc aaa aac agt ccc acc ctg ttt gat gag gca ctg cgc aga gac cta      720
114 Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu Arg Arg Asp Leu
115 225             230             235                 240
117 gca gac ttc cgg atc cag cac cca gac ttg atc ctg cta cag tac gta      768
118 Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val
119            245             250             255
121 gat gac tta ctg ctg gcc gcc act tct gag ctc gac tgc caa caa ggt      816
122 Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly
123            260             265             270
125 act cgg gcc ctg tta caa acc cta gga gac ctc ggg tat cgg gcc tcg      864
126 Thr Arg Ala Leu Leu Gln Thr Leu Gly Asp Leu Gly Tyr Arg Ala Ser
127            275             280             285
129 gcc aag aaa gcc caa att tgc cag aaa cag gtc aag tat ctg ggg tat      912
130 Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr
131      290             295             300
133 ctt cta aaa gag ggt cag aga tgg ctg act gag gcc aga aaa gag act      960
134 Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr
135 305             310             315                 320
137 gtg atg ggg cag cct act ccg aag acc ccg cgg caa cta agg gag ttc     1008
138 Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe
139            325             330             335
141 cta ggg acg gca ggc ttc tgt cgc ctc tgg atc cct ggg ttt gca gaa     1056
142 Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu
143            340             345             350
145 atg gca gcc ccc ttg tac cct ctc acc aaa acg ggg act ctg ttt aat     1104
146 Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn
147            355             360             365
149 tgg ggc cca gac caa caa aag gcc tat caa gaa atc aag caa gct ctt     1152
150 Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu
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Input Set : A:\Sequence Listing.txt
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151     370                375                 380
153 cta act gcc cca gcc ctg ggg ttg cca gat ttg act aag ccc ttt gaa     1200
154 Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu
155 385                390                 395                 400
157 ctc ttt gtc gac gag aag cag ggc tac gcc aaa ggt gtc cta acg caa     1248
158 Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln
159                405                410                 415
161 aaa ctg gga cct tgg cgt cgg ccg gtg gcc tac ctg tcc aaa aag cta     1296
162 Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu
163                420                425                 430
165 gac cca gta gca gct ggg tgg ccc cct tgc cta cgg atg gta gca gcc     1344
166 Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala
167         435                440                 445
169 att gcc gta ctg aca aag gat gca ggc aag cta acc atg gga cag cca     1392
170 Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro
171     450                455                 460
173 cta gtc att ctg gcc ccc cat gca gta gag gca cta gtc aaa caa ccc     1440
174 Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro
175 465                470                 475                 480
177 ccc gat cga tgg ctt tcc aac gcc cgg atg act cac tat cag gcc ttg     1488
178 Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu
179                485                490                 495
181 ctt ttg gac acg gac cgg gtc cag ttc gga ccg gtg gta gcc ctg aac     1536
182 Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn
183                500                505                 510
185 ccg gct aca ctg ctc cca ctg cct gag gaa ggg ctg cag cac aac tgc     1584
186 Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys
187         515                520                 525
189 ctt gat atc ctg gcc gaa gcc cac gga acc cga ccc gac cta acg gac     1632
190 Leu Asp Ile Leu Ala Glu Ala His Gly Thr Arg Pro Asp Leu Thr Asp
191     530                535                 540
193 cag ccg ctc cca gac gcc gac cac acc tgg tac acg ggt gga tcc agt     1680
194 Gln Pro Leu Pro Asp Ala Asp His Thr Trp Tyr Thr Gly Gly Ser Ser
195 545                550                 555                 560
197 ctc ttg caa gag gga cag cgt aag gcg gga gct gcg gtg acc acc gag     1728
198 Leu Leu Gln Glu Gly Gln Arg Lys Ala Gly Ala Ala Val Thr Thr Glu
199                565                570                 575
201 acc gag gta atc tgg gct aaa gcc ctg cca gcc ggg aca tcc gct cag     1776
202 Thr Glu Val Ile Trp Ala Lys Ala Leu Pro Ala Gly Thr Ser Ala Gln
203                580                585                 590
205 cgg gct cag ctg ata gca ctc acc cag gcc cta agg atg gca gaa ggt     1824
206 Arg Ala Gln Leu Ile Ala Leu Thr Gln Ala Leu Arg Met Ala Glu Gly
207         595                600                 605
209 aag aag cta aat gtt tat acg aat tcc cgt tat gct ttt gct act gcc     1872
210 Lys Lys Leu Asn Val Tyr Thr Asn Ser Arg Tyr Ala Phe Ala Thr Ala
211     610                615                 620
213 cat atc cat gga gaa ata tac aga agg cgt ggg ttg ctc aca tca gaa     1920
214 His Ile His Gly Glu Ile Tyr Arg Arg Arg Gly Leu Leu Thr Ser Glu
215 625                630                635                 640
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217 ggc aaa gag atc aaa aat aag gac gag ata ttg gcc cta cta aaa gcc      1968
218 Gly Lys Glu Ile Lys Asn Lys Asp Glu Ile Leu Ala Leu Leu Lys Ala
219                 645             650             655
221 ctc ttt ctg ccc aaa aga ctt agc ata atc cat tgt cca gga cat caa      2016
222 Leu Phe Leu Pro Lys Arg Leu Ser Ile Ile His Cys Pro Gly His Gln
223             660             665             670
225 aag gga cac agc gcc gag gct aga ggc aac cgg atg gct gac caa gcg      2064
226 Lys Gly His Ser Ala Glu Ala Arg Gly Asn Arg Met Ala Asp Gln Ala
227         675             680             685
229 gcc cga aag gca gcc atc aca gag aat cca gac acc tct acc ctc ctc      2112
230 Ala Arg Lys Ala Ala Ile Thr Glu Asn Pro Asp Thr Ser Thr Leu Leu
231     690             695             700
233 ata gaa aat tca tca ccc aat tcc cgc tta att aat taa               2151
234 Ile Glu Asn Ser Ser Pro Asn Ser Arg Leu Ile Asn
235 705             710             715
238 <210> SEQ ID NO: 2
240 <211> LENGTH: 716
242 <212> TYPE: PRT
244 <213> ORGANISM: Moloney-Murine Leukemia Virus
247 <400> SEQUENCE: 2
249 Met Gly Gly Ser His His His His His His Gly Met Ala Ser Met Thr
250 1           5               10              15
253 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys His
254             20              25              30
257 Met Thr Leu Asn Ile Glu Asp Glu Tyr Arg Leu His Glu Thr Ser Lys
258         35              40              45
261 Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
262     50              55              60
265 Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro
266 65              70              75              80
269 Leu Ile Ile Leu Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
270             85              90              95
273 Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
274             100             105             110
277 Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn
278         115             120             125
281 Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro
282     130             135             140
285 Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro
286 145             150             155             160
289 Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His
290             165             170             175
293 Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg
294             180             185             190
297 Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro
298         195             200             205
301 Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly
302     210             215             220
305 Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu Arg Arg Asp Leu
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306 225                     230                     235                     240
309 Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val
310             245                     250                     255
313 Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly
314             260                     265                     270
317 Thr Arg Ala Leu Leu Gln Thr Leu Gly Asp Leu Gly Tyr Arg Ala Ser
318             275                     280                     285
321 Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr
322         290                     295                     300
325 Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr
326 305                     310                     315                     320
329 Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe
330                 325                     330                     335
333 Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu
334             340                     345                     350
337 Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn
338         355                     360                     365
341 Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu
342     370                     375                     380
345 Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu
346 385                     390                     395                     400
349 Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln
350             405                     410                     415
353 Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu
354             420                     425                     430
357 Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala
358             435                     440                     445
361 Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro
362     450                     455                     460
365 Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro
366 465                     470                     475                     480
369 Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu
370             485                     490                     495
373 Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn
374             500                     505                     510
377 Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys
378         515                     520                     525
381 Leu Asp Ile Leu Ala Glu Ala His Gly Thr Arg Pro Asp Leu Thr Asp
382     530                     535                     540
385 Gln Pro Leu Pro Asp Ala Asp His Thr Trp Tyr Thr Gly Gly Ser Ser
386 545                     550                     555                     560
389 Leu Leu Gln Glu Gly Gln Arg Lys Ala Gly Ala Ala Val Thr Thr Glu
390             565                     570                     575
393 Thr Glu Val Ile Trp Ala Lys Ala Leu Pro Ala Gly Thr Ser Ala Gln
394             580                     585                     590
397 Arg Ala Gln Leu Ile Ala Leu Thr Gln Ala Leu Arg Met Ala Glu Gly
398         595                     600                     605
401 Lys Lys Leu Asn Val Tyr Thr Asn Ser Arg Tyr Ala Phe Ala Thr Ala
402         610                     615                     620
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/18/2004
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Input Set : **A:\Sequence Listing.txt**
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.**Invalid <213> Response:**
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5

VERIFICATION SUMMARY   DATE: 10/18/2004
PATENT APPLICATION: US/09/845,157A   TIME: 10:38:03

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